#2 0590
10/09 OIPE

RAW SEQUENCE LISTING   DATE: 06/08/2001
PATENT APPLICATION: US/09/841,805   TIME: 11:46:26

Input Set : **C:\PAOLA\09841805.txt**
Output Set: **N:\CRF3\06082001\I841805.raw**

SEQUENCE LISTING   **ENTERED**

```
 3 (1) GENERAL INFORMATION:
 5      (i) APPLICANT: Lal, Preeti
 6                    Shah, Purvi
 7                    Corley, Neil C.
 9     (ii) TITLE OF INVENTION: HUMAN MEMBRANE RECYCLING
10                             PROTEINS
12    (iii) NUMBER OF SEQUENCES: 5
14     (iv) CORRESPONDENCE ADDRESS:
15          (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
16          (B) STREET: 3174 Porter Dr.
17          (C) CITY: Palo Alto
18          (D) STATE: CA
19          (E) COUNTRY: USA
20          (F) ZIP: 94304
22      (v) COMPUTER READABLE FORM:
23          (A) MEDIUM TYPE: Diskette
24          (B) COMPUTER: IBM Compatible
25          (C) OPERATING SYSTEM: DOS
26          (D) SOFTWARE: FastSEQ for Windows Version 2.0
28     (vi) CURRENT APPLICATION DATA:
29          (A) APPLICATION NUMBER: US/09/841,805
30          (B) FILING DATE: 24-Apr-2001
31          (C) CLASSIFICATION:
33    (vii) PRIOR APPLICATION DATA:
34          (A) APPLICATION NUMBER: 09/360,125
35          (B) FILING DATE:
37   (viii) ATTORNEY/AGENT INFORMATION:
38          (A) NAME: Billings, Lucy J.
39          (B) REGISTRATION NUMBER: 36,749
40          (C) REFERENCE/DOCKET NUMBER: PF-0456 US
42     (ix) TELECOMMUNICATION INFORMATION:
43          (A) TELEPHONE: 650-855-0555
44          (B) TELEFAX: 650-845-4166
47 (2) INFORMATION FOR SEQ ID NO: 1:
49      (i) SEQUENCE CHARACTERISTICS:
50          (A) LENGTH: 347 amino acids
51          (B) TYPE: amino acid
52          (C) STRANDEDNESS: single
53          (D) TOPOLOGY: linear
55    (vii) IMMEDIATE SOURCE:
56          (A) LIBRARY: TONGTUT01
57          (B) CLONE: 980615
59      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
61 Met Ala Gln Ser Arg Asp Gly Gly Asn Pro Phe Ala Glu Pro Ser Glu
62 1               5                   10                  15
63 Leu Asp Asn Pro Phe Gln Asp Pro Ala Val Ile Gln His Arg Pro Ser
```

C--> 29 and C--> 30 markers appear beside lines 29 and 30.

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```
64              20              25                  30
65  Arg Gln Tyr Ala Thr Leu Asp Val Tyr Asn Pro Phe Glu Thr Arg Glu
66          35              40                  45
67  Pro Pro Pro Ala Tyr Glu Pro Pro Ala Pro Ala Pro Leu Pro Pro Pro
68          50              55                  60
69  Ser Ala Pro Ser Leu Gln Pro Ser Arg Lys Leu Ser Pro Thr Glu Pro
70  65              70                  75                  80
71  Lys Asn Tyr Gly Ser Tyr Ser Thr Gln Ala Ser Ala Ala Ala Ala Thr
72              85                  90                  95
73  Ala Glu Leu Leu Lys Lys Gln Glu Glu Leu Asn Arg Lys Ala Glu Glu
74          100                 105                 110
75  Leu Asp Arg Arg Glu Arg Glu Leu Gln His Ala Ala Leu Gly Gly Thr
76          115                 120                 125
77  Ala Thr Arg Gln Asn Asn Trp Pro Pro Leu Pro Ser Phe Cys Pro Val
78          130             135                 140
79  Gln Pro Cys Phe Phe Gln Asp Ile Ser Met Glu Ile Pro Gln Glu Phe
80  145             150                 155                 160
81  Gln Lys Thr Val Ser Thr Met Tyr Tyr Leu Trp Met Cys Ser Thr Leu
82              165                 170                 175
83  Ala Leu Leu Leu Asn Phe Leu Ala Cys Leu Ala Ser Phe Cys Val Glu
84          180                 185                 190
85  Thr Asn Asn Gly Ala Gly Phe Gly Leu Ser Ile Leu Trp Val Leu Leu
86          195                 200                 205
87  Phe Thr Pro Cys Ser Phe Val Cys Trp Tyr Arg Pro Met Tyr Lys Ala
88          210             215                 220
89  Phe Arg Ser Asp Ser Ser Phe Asn Phe Phe Val Phe Phe Ile Phe
90  225             230                 235                 240
91  Phe Val Gln Asp Val Leu Phe Val Leu Gln Ala Ile Gly Ile Pro Gly
92              245                 250                 255
93  Trp Gly Phe Ser Gly Trp Ile Ser Ala Leu Val Val Pro Lys Gly Asn
94              260                 265                 270
95  Thr Ala Val Ser Val Leu Met Leu Leu Val Ala Leu Leu Phe Thr Gly
96          275             280                 285
97  Ile Ala Val Leu Gly Ile Val Met Leu Lys Arg Ile His Ser Leu Tyr
98          290             295                 300
99  Arg Arg Thr Gly Ala Ser Phe Gln Lys Ala Gln Gln Glu Phe Ala Ala
100 305             310                 315                 320
101 Gly Val Phe Ser Asn Pro Ala Val Arg Thr Ala Ala Ala Asn Ala Ala
102              325                 330                 335
103 Ala Gly Ala Ala Glu Asn Ala Phe Arg Ala Pro
104          340             345
```

106 (2) INFORMATION FOR SEQ ID NO: 2:
108   (i) SEQUENCE CHARACTERISTICS:
109   (A) LENGTH: 1521 base pairs
110   (B) TYPE: nucleic acid
111   (C) STRANDEDNESS: single
112   (D) TOPOLOGY: linear
114   (vii) IMMEDIATE SOURCE:
115   (A) LIBRARY: TONGTUT01

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```
116              (B) CLONE: 980615
118     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
120  NGACGCAGGC GCAACCCACG GCTGCTGCGG GGATCCTTGT GGCCCTTCCG GTCGATGGAA      60
121  CCAATCCGTG CACAGAGAAG CGGGGCGAAC TGAGGCGAGT GAAGTGGACT CTGAGGGCTA     120
122  CCGCTACCGC CACTGCTGCG GCAGGGGCGT GGAGGGCAGA GGGCCGCGGA GGCCGCAGTT     180
123  GCAAACATGG CTCAGAGCAG AGACGGCGGA AACCCGTTCG CCGAGCCCAG CGAGCTTGAC     240
124  AACCCCTTTC AGGACCCAGC TGTGATCCAG CACCGACCCA GCCGGCAGTA TGCCACGCTT     300
125  GACGTCTACA ACCCTTTTGA GACCCGGGAG CCACCACCAG CCTATGAGCC TCCAGCCCCT     360
126  GCCCCATTGC CTCCACCCTC AGCTCCCTCC TTGCAGCCCT CGAGAAAGCT CAGCCCCACA     420
127  GAACCTAAGA ACTATGGCTC ATACAGCACT CAGGCCTCAG CTGCAGCAGC CACAGCTGAG     480
128  CTGCTGAAGA AACAGGAGGA GCTCAACCGG AAGGCAGAGG AGTTGGACCG AAGGGAGCGA     540
129  GAGCTGCAGC ATGCTGCCCT GGGGGGCACA GCTACTCGAC AGAACAATTG GCCCCCTCTA     600
130  CCTTCTTTTT GTCCAGTTCA GCCCTGCTTT TTCCAGGACA TCTCCATGGA GATCCCCCAA     660
131  GAATTTCAGA AGACTGTATC CACCATGTAC TACCTCTGGA TGTGCAGCAC GCTGGCTCTT     720
132  CTCCTGAACT TCCTCGCCTG CCTGGCCAGC TTCTGTGTGG AAACCAACAA TGGCGCAGGC     780
133  TTTGGGCTTT CTATCCTCTG GGTCCTCCTT TTCACTCCCT GCTCCTTTGT CTGCTGGTAC     840
134  CGCCCCATGT ATAAGGCTTT CCGGAGTGAC AGTTCATTCA ATTTCTTCGT TTTCTTCTTC     900
135  ATTTTCTTCG TCCAGGATGT GCTCTTTGTC CTCCAGGCCA TTGGTATCCC AGGTTGGGGA     960
136  TTCAGTGGCT GGATCTCTGC TCTGGTGGTG CCGAAGGGCA ACACAGCAGT ATCCGTGCTC    1020
137  ATGCTGCTGG TCGCCCTGCT CTTCACTGGC ATTGCTGTGC TAGGAATTGT CATGCTGAAA    1080
138  CGGATCCACT CCTTATACCG CCGCACAGGT GCCAGCTTTC AGAAGGCCCA GCAAGAATTT    1140
139  GCTGCTGGTG TCTTCTCCAA CCCTGCGGTG CGAACCGCAG CTGCCAATGC AGCCGCTGGG    1200
140  GCTGCTGAAA ATGCCTTCCG GGCCCCGTGA CCCCTGACTG GGATGCCCTG GCCCTGCTAC    1260
141  TTGAGGGAGC TGACTTAGCT CCCGTCCCTA AGGTCTCTGG GACTTGGAGA GACATCACTA    1320
142  ACTGATGGCT CCTCCGTAGT GCTCCCAATC CTATGGCCAT GACTGCTGAA CCTGACAGGC    1380
143  GTGTGGGGAG TTCACTGTGA CCTAGTCCCC CCATCAGGCC ACACTGCTGC CACCTCTCAC    1440
144  ACGCCCCAAC CCAGCTTCCC TCTGCTGTGC CACGGCTGTT GCTTCGGTTA TTTAAATAAA    1500
145  AAGAAAGTGG AACTGGAACT G                                              1521
147  (2) INFORMATION FOR SEQ ID NO: 3:
149        (i) SEQUENCE CHARACTERISTICS:
150            (A) LENGTH: 329 amino acids
151            (B) TYPE: amino acid
152            (C) STRANDEDNESS: single
153            (D) TOPOLOGY: linear
155      (vii) IMMEDIATE SOURCE:
156            (A) LIBRARY: BRSTNOT01
157            (B) CLONE: 412453
159       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
161  Met Ser Ala Phe Asp Thr Asn Pro Phe Ala Asp Pro Val Asp Val Asn
162    1               5                  10                  15
163  Pro Phe Gln Asp Pro Ser Val Thr Gln Leu Thr Asn Ala Pro Gln Gly
164            20                  25                  30
165  Gly Leu Ala Glu Phe Asn Pro Phe Ser Glu Thr Asn Ala Ala Thr Thr
166            35                  40                  45
167  Val Pro Val Thr Gln Leu Pro Gly Ser Ser Gln Pro Ala Val Leu Gln
168        50                  55                  60
169  Pro Ser Val Glu Pro Thr Gln Pro Thr Pro Gln Ala Val Val Ser Ala
170  65                  70                  75                  80
171  Ala Gln Ala Gly Leu Leu Arg Gln Gln Glu Glu Leu Asp Arg Lys Ala
```

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```
172                     85              90              95
173  Ala Glu Leu Glu Arg Lys Glu Arg Glu Leu Gln Asn Thr Val Ala Asn
174              100             105             110
175  Leu His Val Arg Gln Asn Asn Trp Pro Pro Leu Pro Ser Trp Cys Pro
176          115             120             125
177  Val Lys Pro Cys Phe Tyr Gln Asp Phe Ser Thr Glu Ile Pro Ala Asp
178      130             135             140
179  Tyr Gln Arg Ile Cys Lys Met Leu Tyr Tyr Leu Trp Met Leu His Ser
180  145             150             155             160
181  Val Thr Leu Phe Leu Asn Leu Leu Ala Cys Leu Ala Trp Phe Ser Gly
182              165             170             175
183  Asn Ser Ser Lys Gly Val Asp Phe Gly Leu Ser Ile Leu Trp Phe Leu
184              180             185             190
185  Ile Phe Thr Pro Cys Ala Phe Leu Cys Trp Tyr Arg Pro Ile Tyr Lys
186          195             200             205
187  Ala Phe Arg Ser Asp Asn Ser Phe Ser Phe Phe Val Phe Phe Phe Val
188      210             215             220
189  Phe Phe Cys Gln Ile Gly Ile Tyr Ile Ile Gln Leu Val Gly Ile Pro
190  225             230             235             240
191  Gly Leu Gly Asp Ser Gly Trp Ile Ala Ala Leu Ser Thr Leu Asp Asn
192              245             250             255
193  His Ser Leu Ala Ile Ser Val Ile Met Met Val Val Ala Gly Phe Phe
194              260             265             270
195  Thr Leu Cys Ala Val Leu Ser Val Phe Leu Leu Gln Arg Val His Ser
196          275             280             285
197  Leu Tyr Arg Arg Thr Gly Ala Ser Phe Gln Gln Ala Gln Glu Glu Phe
198      290             295             300
199  Ser Gln Gly Ile Phe Ser Ser Arg Thr Phe His Arg Ala Ala Ser Ser
200  305             310             315             320
201  Ala Ala Gln Gly Ala Phe Gln Gly Asn
202              325
204  (2) INFORMATION FOR SEQ ID NO: 4:
206      (i) SEQUENCE CHARACTERISTICS:
207          (A) LENGTH: 2434 base pairs
208          (B) TYPE: nucleic acid
209          (C) STRANDEDNESS: single
210          (D) TOPOLOGY: linear
212     (vii) IMMEDIATE SOURCE:
213          (A) LIBRARY: BRSTNOT01
214          (B) CLONE: 412453
216     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
218  NCCGGAAGTG GAGGGTCTAC ACGAAGCGCC GCTGGGTCTG GGTGCCCGGA GGCAGCAGCG      60
219  TTCGCGGAGT TCGCCCGCTG GCCCCCGATC ACCATGTCGG CTTTCGACAC CAACCCCTTC     120
220  GCGGACCCAG TGGATGTAAA CCCCTTCCAG GATCCCTCTG TGACCCAGCT GACCAACGCC     180
221  CCGCAGGGCG GCCTGGCGGA ATTCAACCCC TTCTCAGAGA CAAATGCAGC GACAACAGTT     240
222  CCTGTCACCC AACTCCCTGG GTCCTCACAG CCAGCGGTTC TCCAGCCATC AGTGGAACCA     300
223  ACCCAGCCGA CCCCCCAGGC CGTGGTGTCT GCAGCCCAGG CAGGCCTGCT CCGGCAGCAG     360
224  GAAGAACTGG ACAGGAAAGC TGCCGAGCTG AACGCAAGG AGCGGGAGCT GCAGAACACT     420
225  GTAGCCAACT TGCATGTGAG ACAGAACAAC TGGCCCCCTC TGCCCTCGTG GTGCCCTGTG     480
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```
226  AAGCCCTGCT TCTATCAGGA TTTCTCCACA GAGATCCCTG CCGACTACCA GCGGATATGC   540
227  AAGATGCTCT ACTATCTGTG GATGTTGCAT TCAGTGACTC TGTTTCTGAA CCTGCTTGCC   600
228  TGCCTGGCCT GGTTCTCGGG CAACAGCTCC AAGGGAGTGG ACTTTGGCCT CTCCATCCTG   660
229  TGGTTTCTGA TCTTCACTCC CTGTGCCTTC CTTTGTTGGT ACCGACCCAT CTATAAGGCC   720
230  TTTAGGTCCG ACAACTCTTT CAGCTTCTTT GTGTTCTTCT TTGTATTTTT TTGTCAAATA   780
231  GGGATCTACA TCATCCAGTT GGTTGGCATC CCTGGCCTGG GGACAGCGG TTGGATTGCA   840
232  GCCCTGTCTA CACTGGATAA TCATTCCCTG GCCATATCAG TCATCATGAT GGTGGTGGCT   900
233  GGCTTCTTCA CCCTCTGTGC CGTGCTCTCA GTCTTCCTCC TGCAGCGGGT GCACTCCCTC   960
234  TACCGACGGA CAGGGGCCAG CTTCCAGCAG GCCCAGGAGG AGTTTTCCCA GGGCATCTTC  1020
235  AGCAGCAGAA CCTTCCACAG AGCTGCTTCA TCTGCTGCCC AAGGAGCCTT CCAGGGGAAT  1080
236  TAGTCCTCCT CTCTTCTCTC CCCCTCAGCC TTTCTCTCGC CTGCCTTCTG AGCTGCACTT  1140
237  TCCGTGGGTG CCTTATGTGG TGGTGGTTGT GCCCAGCACA GACCTGGCAG GGTTCTTGCC  1200
238  GTGGCTCTTC CTCCTCCCTC AGCGACCAGC TCTCCCTGGA ACGGGAGGGA CAGGGAATTT  1260
239  TTTCCCCCTC TATGTACAAA AAAAAACAAA GCTCTCTTTC CTTCTCTGGT GATGGTTTGG  1320
240  TAGGATTCTT TTGTCTCTGG AAGCAGTGGG ACTGAAGTTC TCTTCGTCCT GTGCACACAC  1380
241  AGACACCCCC ACACAGTTGG GATCACAGGC TGACCTGGGC CCATCCCAGC TGGAGCTTTC  1440
242  TGCCAGGGTC CTGGGCCTTG ACTCCCCCAC CCTGCAGGCC TGGCCTGAAT CTGGCTTCTT  1500
243  AGACACAGCC CAGTCCTTCC TGCCTGGGCT GGGAATAAGC CTCTCACAGG TTCTGGTGGA  1560
244  CAGATCTGTT CCCCAGGTCA CTCCAGTGGT CTCCAGGCTT CCAGAGAAGG CTGGTTGCCT  1620
245  CAAGCTCTTC TCTGCCTCAT AAACGGATCC AGAGAAGGCT GGTTGCCTTA AGCTCTTCCC  1680
246  TGCCTCGTGT TCCTGAGAAA CGGATTAATA GCCCTTTATC CCCCTGCACC CTCCTGCAGG  1740
247  GGATGGCACT TTGAGCCCTC TGGAGCCCTC CCCTTGCTGA GCCTTACTCT CTTCAGACTT  1800
248  TCTGAATGTA CAGTGCCGTT GGTTGGGATT TGGGGACTGG AAGGGACCAA GGACACTGAC  1860
249  CCCAAGCTGT CCTGCCTAGC GTCCAGCGTC TTCTAGGAGG GTGGGGTCTG CCTGTCCTGG  1920
250  TGTGGTTGGT TTGGCCCTGT TTGCTGTGAC TACCCCCCCC CCTCCCCGAA CCGAGGGACG  1980
251  GCTGCCTTTG TCTCTGCCTC AGATGCCACC TGCCCCGCCC ATGCTCCCCA TCAGCAGCAT  2040
252  CCAGACTTTC AGGAAGGGCA GGACCAGCCA GTCCAGAACC GCATCCCTCA GCAGGGACTG  2100
253  ATAAGCCATC TCTCGGAGGG CCCCCTAATA CCCAGTGGAG TCTGGTTCAC ACCCTGGGGG  2160
254  GTGTGTCACT GTGATGGGAC ACGTAGGAGT CCACCCTTAA AACCAGCACC CTGTCCCTCG  2220
255  AGGCTGCCGA GTGGGTGTGT GGACTGGGGT GCCTTCCCAC AAAACTAGCC TCCGGCTCTG  2280
256  GGCCCGAGAC AGCCGCAGGC CCCAGCCACT GAATGATACT GGCAGCGGCT GGGGTTTTAT  2340
257  GAACTCCTTT CTGGTATTTT TTCCCCTCTA TGTACAAATG TATATGTTAC GTCTCAATTT  2400
258  TTGTGCTTAA GTAAAAATAA AAACATTTTC AGAC                               2434
```

```
260  (2) INFORMATION FOR SEQ ID NO: 5:
262      (i) SEQUENCE CHARACTERISTICS:
263          (A) LENGTH: 338 amino acids
264          (B) TYPE: amino acid
265          (C) STRANDEDNESS: single
266          (D) TOPOLOGY: linear
268     (vii) IMMEDIATE SOURCE:
269          (A) LIBRARY: GenBank
270          (B) CLONE: 487057
272     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
274  Met Ser Asp Phe Asp Ser Asn Pro Phe Ala Asp Pro Asp Leu Asn Asn
275   1                5                10               15
276  Pro Phe Lys Asp Pro Ser Val Thr Gln Val Thr Arg Asn Val Pro Pro
277               20                25                30
278  Gly Leu Asp Glu Tyr Asn Pro Phe Ser Asp Ser Arg Thr Pro Pro Pro
279           35               40                45
```

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Input Set : **C:\PAOLA\09841805.txt**
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L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]